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# UniProtKB/Swiss-Prot entry O75844

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Entry history

[Entry info] [Name and origin] [References] [Comments] [Cross-references] [Keywords] [Features] [Sequence] [Tools]

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## Entry information

| | |
|---|---|
| Entry name | FACE1_HUMAN |
| Primary accession number | O75844 |
| Secondary accession numbers | Q8NDZ8 Q9UBQ2 |
| Integrated into Swiss-Prot on | July 15, 1999 |
| Sequence was last modified on | April 27, 2001 (Sequence version 2) |
| Annotations were last modified on | September 2, 2008 (Entry version 78) |

## Name and origin of the protein

| | |
|---|---|
| Protein name | CAAX prenyl protease 1 homolog |
| Synonyms | EC 3.4.24.84<br>Prenyl protein-specific endoprotease 1<br>Farnesylated proteins-converting enzyme 1<br>FACE-1<br>Zinc metalloproteinase Ste24 homolog |
| Gene name | Name: ZMPSTE24<br>Synonyms: FACE1, STE24 |
| From | Homo sapiens (Human) [TaxID: 9606] |
| Taxonomy | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo. |
| Protein existence | 1: Evidence at protein level; |

## References

[1] NUCLEOTIDE SEQUENCE [MRNA].
TISSUE=Brain;
DOI=10.1016/S0304-4165(98)00170-6; PubMed=10076063 [NCBI, ExPASy, EBI, Israel, Japan]
Kumagai H., Kawamura Y., Yanagisawa K., Komano H.;
"Identification of a human cDNA encoding a novel protein structurally related to the yeast membrane-associated metalloprotease, Ste24p.";
Biochim. Biophys. Acta 1426:468-474(1999).

[2] NUCLEOTIDE SEQUENCE [MRNA].
TISSUE=B-cell, and Fetal brain;
DOI=10.1083/jcb.142.3.635; PubMed=9700155 [NCBI, ExPASy, EBI, Israel, Japan]
Tam A., Nouvet F.J., Fujimura-Kamada K., Slunt H., Sisodia S.S., Michaelis S.;
"Dual roles for Ste24p in yeast a-factor maturation: NH2-terminal proteolysis and COOH-terminal CAAX processing.";
J. Cell Biol. 142:635-649(1998).

[3] NUCLEOTIDE SEQUENCE [MRNA].
TISSUE=Ovary;
DOI=10.1006/geno.1999.5834; PubMed=10373325 [NCBI, ExPASy, EBI, Israel, Japan]
Freije J.M.P., Blay P., Pendas A.M., Cadinanos J., Crespo P., Lopez-Otin C.;
"Identification and chromosomal location of two human genes encoding enzymes potentially involved in proteolytic maturation of farnesylated proteins.";
Genomics 58:270-280(1999).

[4] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
DOI=10.1038/nature04727; PubMed=16710414 [NCBI, ExPASy, EBI, Israel, Japan]
Gregory S.G., Barlow K.F., McLay K.E., Kaul R., Swarbreck D., Dunham A., Scott C.E., Howe K.L., Woodfine K., Spencer C.C.A., Jones M.C., Gillson C., Searle S., Zhou Y., Kokocinski F., McDonald L., Evans R., Phillips K., Atkinson A., [redacted], Bentley D.R.;
"The DNA sequence and biological annotation of human chromosome 1.";
Nature 441:315-321(2006).

[5] NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA], AND VARIANT ALA-137.
TISSUE=Testis;
DOI=10.1101/gr.2596504; PubMed=15489334 [NCBI, ExPASy, EBI, Israel, Japan]
The MGC Project Team;
"The status, quality, and expansion of the NIH full-length cDNA project: the Mammalian Gene Collection (MGC).";
Genome Res. 14:2121-2127(2004).

[6] VARIANT MADB ARG-340.
DOI=10.1093/hmg/ddg213; PubMed=12913070 [NCBI, ExPASy, EBI, Israel, Japan]
Agarwal A.K., Fryns J.-P., Auchus R.J., Garg A.;
"Zinc metalloproteinase, ZMPSTE24, is mutated in mandibuloacral dysplasia.";
Hum. Mol. Genet. 12:1995-2001(2003).

[7] INVOLVEMENT IN LETHAL TIGHT SKIN CONTRACTURE SYNDROME.
DOI=10.1093/hmg/ddh265; PubMed=15317753 [NCBI, ExPASy, EBI, Israel, Japan]
Navarro C.L., De Sandre-Giovannoli A., Bernard R., Boccaccio I., Boyer A., Genevieve D., Hadj-Rabia S., Gaudy-Marqueste C., Smitt H.S., Vabres P., Faivre L., Verloes A., Van Essen T., Flori E., Hennekam R., Beemer F.A., Laurent N., Le Merrer M., Cau P., Levy N.;
"Lamin A and ZMPSTE24 (FACE-1) defects cause nuclear disorganization and identify restrictive dermopathy as a lethal neonatal laminopathy.";
Hum. Mol. Genet. 13:2493-2503(2004).

Comments

- *FUNCTION*: Proteolytically removes the C-terminal three residues of farnesylated proteins. Acts on lamin A/C.
- *CATALYTIC ACTIVITY*: The peptide bond hydrolyzed can be designated -C-|-A-A-X in which C is an S-isoprenylated cysteine residue, A is usually aliphatic and X is the C-terminal residue of the substrat protein, and may be any of several amino acids.
- *COFACTOR*: Binds 1 zinc ion per subunit *(By similarity)*.
- *SUBCELLULAR LOCATION*: Endoplasmic reticulum membrane; Multi-pass membrane protein. Gol apparatus membrane; Multi-pass membrane protein *(Probable)*.
- *TISSUE SPECIFICITY*: Widely expressed. High levels in kidney, prostate, testis and ovary.
- *DISEASE*: Defects in ZMPSTE24 are the cause of mandibuloacral dysplasia with type B lipodystroph

(MADB) [MIM:608612]. Mandibuloacral dysplasia (MAD) is a rare autosomal recessive disorder characterized by mandibular and clavicular hypoplasia, acroosteolysis, delayed closure of the cranial suture, joint contractures, and types A or B patterns of lipodystrophy. Type B lipodystrophy observed MADB, is characterized by generalized fat loss.

- *DISEASE*: Defects in ZMPSTE24 are a cause of lethal tight skin contracture syndrome [MIM:275210] also called restrictive dermopathy (RD). Lethal tight skin contracture syndrome is a rare disorder mainly characterized by intrauterine growth retardation, tight and rigid skin with erosions, prominent superficial vasculature and epidermal hyperkeratosis, facial features (small mouth, small pinched nos and micrognathia), sparse/absent eyelashes and eyebrows, mineralization defects of the skull, thin dysplastic clavicles, pulmonary hypoplasia, multiple joint contractures and an early neonatal lethal course. Liveborn children usually die within the first week of life. The overall prevalence of consanguineous cases suggested an autosomal recessive inheritance.
- *SIMILARITY*: Belongs to the peptidase M48A family [view classification].
- *WEB RESOURCE*: Name=GeneReviews; URL="http://www.genetests.org/query?gene=ZMPSTE24"



Cross-references

Sequence databases

| | | |
|---|---|---|
| EMBL | AB016068; BAA33727.1; -; mRNA. | [EMBL / GenBank / DDBJ] [CoDingSequence] |
| | AF064867; AAC68866.1; -; mRNA. | [EMBL / GenBank / DDBJ] [CoDingSequence] |
| | Y13834; CAB46277.1; -; mRNA. | [EMBL / GenBank / DDBJ] [CoDingSequence] |
| | AL050341; CAB81610.1; -; Genomic_DNA. | [EMBL / GenBank / DDBJ] [CoDingSequence] |
| | BC037283; AAH37283.1; -; mRNA. | [EMBL / GenBank / DDBJ] [CoDingSequence] |
| RefSeq | NP_005848.2; -. | |
| UniGene | Hs.132642 | |

3D structure databases

| | |
|---|---|
| ModBase | O75844. |

Protein-protein interaction databases

| | |
|---|---|
| IntAct | O75844; -. |

Protein family/group databases

| | |
|---|---|
| MEROPS | M48.003; -. |

Organism-specific databases

| | |
|---|---|
| H-InvDB | HIX0000469; -. |
| HGNC | HGNC:12877; ZMPSTE24. |
| GenAtlas | ZMPSTE24. |
| HPA | HPA006988; -. |
| MIM | 275210; phenotype. [NCBI / EBI]<br>606480; gene. [NCBI / EBI]<br>608612; phenotype. [NCBI / EBI] |
| Orphanet | 1662; Dermopathy restrictive lethal.<br>2457; Mandibuloacral dysplasia. |
| PharmGKB | PA37466; -. |
| GeneCards | O75844. |

Gene expression databases

| | |
|---|---|
| ArrayExpress | O75844; -. |
| CleanEx | HS_ZMPSTE24; -. |
| GermOnline | ENSG00000084073; Homo sapiens. |

Ontologies

| | |
|---|---|
| | GO:0008235; Molecular function: metalloexopeptidase activity *(traceable author statement from ProtInc).* |
| GO | GO:0006508; Biological process: proteolysis *(traceable author statement from ProtInc).* |
| | QuickGo view. |

Family and domain databases

| | |
|---|---|
| InterPro | IPR006025; Pept_M_Zn_BS.<br>IPR001915; Peptidase_M48.<br>Graphical view of domain structure. |
| Pfam | PF01435; Peptidase_M48; 1.<br>Pfam graphical view of domain structure. |
| PROSITE | PS00142; ZINC_PROTEASE; FALSE_NEG. |
| BLOCKS | O75844. |

Proteomic databases

| | |
|---|---|
| PeptideAtlas | O75844; -. |

Genome annotation databases

| | |
|---|---|
| Ensembl | ENSG00000084073; Homo sapiens. [Contig view] |
| GeneID | 10269; -. |
| KEGG | hsa:10269; -. |

Phylogenomic databases

| | |
|---|---|
| HOGENOM | O75844; -. |
| HOVERGEN | O75844; -. |

Other

| | |
|---|---|
| SOURCE | ZMPSTE24; Homo sapiens. |
| ProtoNet | O75844. |
| UniRef | View cluster of proteins with at least 50% / 90% / 100% identity. |

Keywords

Disease mutation; Endoplasmic reticulum; Golgi apparatus; Hydrolase; Membrane; Metal-binding; Metalloprotease; Polymorphism; Protease; Transmembrane; Zinc.

Features

 Feature table viewer

 Feature aligner

| Key | From | To | Length | Description | FTId |
|---|---|---|---|---|---|
| CHAIN | 1 | 475 | 475 | CAAX prenyl protease 1 homolog. | PRO_0000138844 |
| TRANSMEM | 19 | 39 | 21 | *Potential.* | |
| TRANSMEM | 82 | 102 | 21 | *Potential.* | |
| TRANSMEM | 124 | 144 | 21 | *Potential.* | |
| TRANSMEM | 171 | 191 | 21 | *Potential.* | |
| TRANSMEM | 196 | 216 | 21 | *Potential.* | |
| TRANSMEM | 348 | 368 | 21 | *Potential.* | |
| TRANSMEM | 383 | 405 | 23 | *Potential.* | |
| ACT_SITE | 336 | 336 | | *By similarity.* | |
| ACT_SITE | 419 | 419 | | Proton donor *(By similarity).* | |
| METAL | 335 | 335 | | Zinc; catalytic *(By similarity).* | |
| METAL | 339 | 339 | | Zinc; catalytic *(By similarity).* | |
| METAL | 415 | 415 | | Zinc; catalytic *(By similarity).* | |
| VARIANT | 137 | 137 | 1 | T -> A (in dbSNP:rs17853725 [NCBI]). | VAR_034711 |
| VARIANT | 340 | 340 | 1 | W -> R (in MADB). | VAR_019308 |

```
CONFLICT    16    16          E -> K (in Ref. 1; BAA33727).
```

Sequence information

Length: 475 AA [This is the length of the unprocessed precursor]

Molecular weight: 54813 Da [This is the MW of the unprocessed precursor]

CRC64: 6C49179DEB0C8F7F [This i a checksum on the sequence]

```
        10         20         30         40         50         60
MGMWASLDAL WEMPAEKRIF GAVLLFSWTV YLWETFLAQR QRRIYKTTTH VPPELGQIMD

        70         80         90        100        110        120
SETFEKSRLY QLDKSTFSFW SGLYSETEGT LILLFGGIPY LWRLSGRFCG YAGFGPEYEI

       130        140        150        160        170        180
TQSLVFLLLA TLFSALTGLP WSLYNTFVIE EKHGFNQQTL GFFMKDAIKK FVVTQCILLP

       190        200        210        220        230        240
VSSLLLYIIK IGGDYFFIYA WLFTLVVSLV LVTIYADYIA PLFDKFTPLP EGKLKEEIEV

       250        260        270        280        290        300
MAKSIDFPLT KVYVVEGSKR SSHSNAYFYG FFKNKRIVLF DTLLEEYSVL NKDIQEDSGM

       310        320        330        340        350        360
EPRNEEEGNS EEIKAKVKNK KQGCKNEEVL AVLGHELGHW KLGHTVKNII ISQMNSFLCF

       370        380        390        400        410        420
FLFAVLIGRK ELFAAFGFYD SQPTLIGLLI IFQFIFSPYN EVLSFCLTVL SRRFEFQADA

       430        440        450        460        470
FAKKLGKAKD LYSALIKLNK DNLGFPVSDW LFSMWHYSHP PLLERLQALK TMKQH
```

O75844 in FASTA format

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*View entry in raw text format (no links)*
*Report form for errors/updates in this UniProtKB/Swiss-Prot entry*

BLAST submission on ExPASy/SIB or at NCBI (USA)

Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

ScanProsite, MotifScan

Submit a homology modeling request to SWISS-MODEL

NPSA Sequence analysis tools

feedback!